

SEQUENCE LISTING

<110> Novozymes A/S

<120> Orotate Transporter Encoding Marker Genes

<130> 10556.204-WO

<160> 22

<170> PatentIn version 3.3

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<212> DNA

<213> Lactococcus lactis

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<221> CDS

<222> (1)..(921)

<223> Orotate transporter encoding ORF

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aat caa aat cca atc aat gcg gat tta cga aaa att gtt ggc tca cca      96
Asn Gln Asn Pro Ile Asn Ala Asp Leu Arg Lys Ile Val Gly Ser Pro
20 25 30

ttt ttg gcc tct gga att tcc aac ttt gtt ggt tcg att ttt tta gga     144
Phe Leu Ala Ser Gly Ile Ser Asn Phe Val Gly Ser Ile Phe Leu Gly
35 40 45

att atc act tta gtg acc agt caa aca ctt ttt cct agt ttt caa ttt     192
Ile Ile Thr Leu Val Thr Ser Gln Thr Leu Phe Pro Ser Phe Gln Phe
50 55 60

gtt ggc tca cac cca gta tgg ata tgg att ggt ggg gtt ctt ggt ggg     240
Val Gly Ser His Pro Val Trp Ile Trp Ile Gly Gly Val Leu Gly Gly
65 70 75 80

att ttt cta aca tct aat gtt tta ctt ttc cca aga tta gga gct gtc     288
Ile Phe Leu Thr Ser Asn Val Leu Leu Phe Pro Arg Leu Gly Ala Val
85 90 95

caa acg gtg att tta cct att ttg ggt cga ata ttg atg ggg aca ctt     336
Gln Thr Val Ile Leu Pro Ile Leu Gly Arg Ile Leu Met Gly Thr Leu
100 105 110

att gat tca ttt ggc tgg ttt cat gcc atg caa ctt ccg atg act ctg     384
Ile Asp Ser Phe Gly Trp Phe His Ala Met Gln Leu Pro Met Thr Leu
115 120 125

atg cgc ttt ttg gga gtt atc att act tta gct ggg gtt att gtc gcg     432
Met Arg Phe Leu Gly Val Ile Ile Thr Leu Ala Gly Val Ile Val Ala
130 135 140

gtt gtt ctt cct aat tta aaa gaa aaa gaa gca gaa acg cac caa act     480
Val Val Leu Pro Asn Leu Lys Glu Lys Glu Ala Glu Thr His Gln Thr
145 150 155 160

aac tta cta ggc tgg cga att tgg gcg gtc atc gtt ggg gca atg tcg     528
Asn Leu Leu Gly Trp Arg Ile Trp Ala Val Ile Val Gly Ala Met Ser
165 170 175

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gct gct caa caa gca att aat ggc aga ttg gga gtt tta ctt gaa aac 576
 Ala Ala Gln Gln Ala Ile Asn Gly Arg Leu Gly Val Leu Leu Glu Asn
 180 185 190

act gca caa gca acc ttt gtt tcg ttc ttc att gga ttt tta gct att 624
 Thr Ala Gln Ala Thr Phe Val Ser Phe Phe Ile Gly Phe Leu Ala Ile
 195 200 205

ttt atc gtg tct ctt ttt att gac cgc cgt ttg cca aaa att tca gaa 672
 Phe Ile Val Ser Leu Phe Ile Asp Arg Arg Leu Pro Lys Ile Ser Glu
 210 215 220

tta aaa aaa gca aaa cct tgg aat gga att ggt gga ttt tta gga gcc 720
 Leu Lys Lys Ala Lys Pro Trp Asn Gly Ile Gly Gly Phe Leu Gly Ala
 225 230 235 240

tca atc gtt ttt gca aca gtc gtt gct gtt ccg caa att ggt gca ggg 768
 Ser Ile Val Phe Ala Thr Val Val Ala Val Pro Gln Ile Gly Ala Gly
 245 250 255

ctg aca att atg atg ggc ttg att gga caa att tta ggc agt atg ttg 816
 Leu Thr Ile Met Met Gly Leu Ile Gly Gln Ile Leu Gly Ser Met Leu
 260 265 270

gtt caa caa ttt ggt tgg tgg cgc tca agt aaa tat ggc att caa att 864
 Val Gln Gln Phe Gly Trp Trp Arg Ser Ser Lys Tyr Gly Ile Gln Ile
 275 280 285

tgg caa att gtt ggg att cta att atg ctg acc gga ata ata ttc att 912
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Phe Leu Ala Ser Gly Ile Ser Asn Phe Val Gly Ser Ile Phe Leu Gly
 35 40 45

Ile Ile Thr Leu Val Thr Ser Gln Thr Leu Phe Pro Ser Phe Gln Phe
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Val Gly Ser His Pro Val Trp Ile Trp Ile Gly Gly Val Leu Gly Gly
 65 70 75 80

Ile Phe Leu Thr Ser Asn Val Leu Leu Phe Pro Arg Leu Gly Ala Val
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Gln Thr Val Ile Leu Pro Ile Leu Gly Arg Ile Leu Met Gly Thr Leu
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 Ile Asp Ser Phe Gly Trp Phe His Ala Met Gln Leu Pro Met Thr Leu
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 Met Arg Phe Leu Gly Val Ile Ile Thr Leu Ala Gly Val Ile Val Ala
 130 135 140
 Val Val Leu Pro Asn Leu Lys Glu Lys Glu Ala Glu Thr His Gln Thr
 145 150 155 160
 Asn Leu Leu Gly Trp Arg Ile Trp Ala Val Ile Val Gly Ala Met Ser
 165 170 175
 Ala Ala Gln Gln Ala Ile Asn Gly Arg Leu Gly Val Leu Leu Glu Asn
 180 185 190
 Thr Ala Gln Ala Thr Phe Val Ser Phe Phe Ile Gly Phe Leu Ala Ile
 195 200 205
 Phe Ile Val Ser Leu Phe Ile Asp Arg Arg Leu Pro Lys Ile Ser Glu
 210 215 220
 Leu Lys Lys Ala Lys Pro Trp Asn Gly Ile Gly Gly Phe Leu Gly Ala
 225 230 235 240
 Ser Ile Val Phe Ala Thr Val Val Ala Val Pro Gln Ile Gly Ala Gly
 245 250 255
 Leu Thr Ile Met Met Gly Leu Ile Gly Gln Ile Leu Gly Ser Met Leu
 260 265 270
 Val Gln Gln Phe Gly Trp Trp Arg Ser Ser Lys Tyr Gly Ile Gln Ile
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